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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	P-13 Div II	Total Pages	21
First Named Inventor or Application Identifier			
Carlos Antonio Durate Cano, et al			
Express Mail Label No.	EL 133 328 919 US		

APPLICATION ELEMENTS
See MPEP chapter 600 concerning utility patent application contents.

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1. ☒ Fee Transmittal Form
(Submit an original, and a duplicate for fee processing)
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(preferred arrangement set forth below)
 - Descriptive title of the invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to Microfiche Appendix
 - Background of the invention
 - Brief Summary of the invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
3. ☒ Drawing(s) (35 USC 113). [Total Sheets: 12]
4. Oath or Declaration [Total Pages: 5]
 - a. ☐ Newly executed (original or copy)
 - b. ☒ Copy from a prior application: (37 CFR 1.63(d))
(for continuation/divisional with Box 17 completed)
(Note: Box 5 below)
 - i. ☐ **DELETION OF INVENTOR(S)**
Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).
5. ☒ Incorporation By Reference (useable if Box 4b is checked)
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. ☐ Microfiche Computer Program (Appendix)
7. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
 - a. ☐ Computer Readable Copy
 - b. ☒ Paper Copy (Identical to computer copy)
 - c. ☒ Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & document(s))
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(when there is an assignee)
10. ☐ English Translation Document (if applicable)
11. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
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9. ☒ Other: Spec. claims, abstract 12 sheets of formal drawings, copy of Declaration and Power of Attorney, Translator's Dec. from parent

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DATE

7-10-2000

1

EXPRESSION SYSTEM OF HETEROLOGOUS ANTIGENS AS FUSION PROTEINS.

Technical Sector.

The present invention is related to the field of the Biotechnology and the genetic engineering, particularly to the expression of heterologous proteins in microbial hosts through their fusion to bacteria peptides, using the technology of the recombinant DNA.

Previous Art.

The usefulness of the technology of the recombinant DNA to produce proteins of any origin in *E. coli* has been extensively demonstrated. For this, an important amount of vectors have been developed, although new variants are necessary due to the fact that, frequently each gene to clone and to express represents an individual case (Denhardt, D.T. and Colasanti, J.; Vectors, Butterworths, Stoneham, M, pp. 179-1987 and Lukacsovich, T. et al., Journal of Biotechnology, 13, 243-1990).

The intracellular synthesis has been the most used strategy for the obtainment of heterologous polypeptides in *E. coli*, due to the high expression levels reachable (Goeddel, D.V, Methods Enzymol., 185, 3-7, 1990). However, factors such as the sensibility to proteases of the host or toxicity of the expressed protein can reduce significantly said levels, independently of the use of regulatory sequences of high efficiency (Reads, C. A. and Saier, M. H., J. Bacteriol., 153, 685-692; Gwyn, G. W., Membrane Protein Expression Systems: To User's Guide, Portland Press, London, UK, 29-82).

The cloning of nucleotide sequences encoding for proteins of interest in suitable vectors, in frame with sequences of nucleic acid that codify stable polypeptides in the host cell, gives rise to the expression of hybrid products in the cytoplasm, known as fusion proteins (Marston, F.A.O., Biochem. J. 240, 119-86). Such polypeptides are generally less sensitive to proteolytic degradation by the host or less toxic due to the formation of inclusion bodies, which results in higher expression levels to those obtained without the use of the stabilizer peptide (Itakura, K. et al., Science, 198, 1056-1977). In addition, this kind of expression facilitates and cheapens the initial steps of the purification if different methods for the subsequent renaturation of the recombinant product are available (Fischer, B., Sumner, I. and Goodenough, P., Biotechnol. Bioeng., 41, 3-13).

The inclusion bodies are insoluble protein aggregates that appear as electrodense bodies in the citosol during the expression of many recombinant proteins in *E. coli* (Rinas, Or. and Bailey, J., Appl. Microbiol. Biotechnol., 37, 609-614). They are the result of the interaction between polypeptides partially folded, whose aggregation is thermodynamically favored due to the exposition, within them, of hydrofobic residues to the solvent (Kiefhaber, T., Rudolph, R. et al., Biotechnology, 9, 825-829). The slow folding in the bacterial citosol of many eukaryotic proteins, due to the abundance of disulphur bridges-forming amino acids (Cystein) or beta-turns forming amino acids (Proline) has stimulated the abundant use of them as stabilizer peptides. Example of the former the use, with this purpose, of polypeptides with binding activity to antibodies, coming from the globulin of the fat of the human milk (HMFG), according to the international patent application PCT No. WO 9207939 A2 920514; from constant regions of the immunoglobulins, as described in the European patent application No. EP 0464533 A1 920108; from the human angiogenin (European patent application No. EP 0423641 A2 910424), of the growth hormone (EP 0429586 A1 910605), the glutation -S-transferase (WO 8809372 A1 881201) and of the swinish adenylate kinase (EP 0423641 A2 910424 and EP 0412526 A2 910213).

However, the use of stabilizer polypeptides that constitute a significant part of the fusion protein has some disadvantages if the former is a vaccine candidate, since the presence of the foreign sequences can alter the natural order of the B and T cell epitopes (Denton, G., Hudecz, F., Kajtár, J. et al., Peptide Research, 7, 258-264) or the processing of the same by the antigen presenting cells (Del Val, M., Schlicht, H., Ruppert, T., et al, Cell, 66, 1145-1153), being able to even to affect seriously the immunogenicity of the candidate by the phenomenon of specific-epitope suppression (Etlinger, H., Immunol. Today, 13, 52-55).

As a result of the aforementioned phenomenon, in some cases, small fragments that still stabilize the expression have been tried to define. For example, the German patent application No. 35 41 856 A1 (Hoechst AG) reports the possibility of using a stabilizer peptide conformed by at least the first 95 amino acids of the N-terminus of the human protein Interleukine (IL-2) to obtain fusion proteins in an insoluble form synthesized in *E. coli*. Similarly in the European Patent Applications No. 0 416 673 A2 and No. 229 998 from the same

company, a stabilizer peptide consistent in the first 58 or 38 amino acids of said protein, is used. In the European patent No. 416 673 B1, the first 58 amino acids of the IL-2 are also used, and a similar strategy is followed, with this purpose, in the case of use of N-terminal fragments of the human seroalbumin (European patent application No. EP 0423641 A1 920212); the activator peptide III of the connective tissue (WO 90136647 A1 901115) and fragments of the human kallikrein (EP 0381433 A1 900808). These inventions give solution to the previous problem, but the fusion polypeptides obtained can not be included in vaccine preparations for being used in human, due to the possibility of induction of autoimmune diseases for the presence in them of homologous or identical sequences to human proteins.

The alternative of using stabilizer polypeptides of bacterial origin --and therefore, without cross reactivity with antigens of human origin-- for intracellular expression, has also been explored with success. One of the most used proteins with this end has been the β -galactosidase of *E. coli* (Itakura, K. et al., Science, 198, 10561977) or portions of it (German patent application No. EP 0235754 A2 870909, of the company Hoechst AG). The principal disadvantage of this system is the great size of this protein which provokes that the desired peptide only represents a small portion of the total hybrid protein (Flowers, N. et al., Appl. Microbiol. Biotechnol. 25, 2671986; Goeddel, D.V. et al., P.N.A.S. USA, 76, 106). Similar problems has presented the use of the C fragment of the tetanus toxoid and the exotoxin of *Pseudomonas* sp. (International Patent Application PCT WO 9403615 A1 940217 and European Patent Application EP 0369316 A2 900523). An expression variant very promissory is the use of fusions with the thioredoxin of *E. coli* (PCT Patent application No. WO 9402502 A1 940203), that uses the property of being liberated from the cell by osmotic stress (Elyaagoubi, A., Kohiyama, M., Richarme, G., J. Bacteriol., 176, 7074 -7078) to facilitate the purification. However, this outline is not functional for the obtainment of inclusion bodies, since the same are not freed through this procedure.

Many of these problems have been solved with the design of modular fusion proteins. In these, the stabilizer peptide is separated from protein of interest by a spacer that permits the independent folding of both, and whose amino acid sequence makes it susceptible to the

attack of specific endopeptidases. If there is a ligand that recognizes the chosen stabilizer, it is possible to purify the fusion polypeptide by affinity chromatography of and finally separate it from the stabilizer through the treatment with different proteases (Cress, D., Shultz, J. and Breitlow, S., Promega you Note, 42, 2-7). An additional advantage is the possibility of exploiting this molecular interaction for the follow-up of intermediate steps of the purification, without the need of antibodies for each protein to express. A well-known example of that is the use of the affinity of the hystidine (Hys) with some metals like the nickel (Ni) and the zinc (Zn) in systems composed by a stabilizer with 6 Hys in tandem and an affinity matrix of nickel chelates, according to what is described in the PCT Patent application No. WO 9115589 A1 911017 of The Upjohn Co. In spite of all this, this kind of expression system does not function in all the cases, since, among other reasons, the protein of interest can have restriction sites for the chosen protease, or be folded so that the spacer is available to the solvent (Uhlen, M. and Moks, T., Meth. Enzymol. 185, 129-140; Cress, D., Shultz, J. and Breitlow, S., Promega you Note, 42, 2-7), to interfere with the binding between the stabilizer and the affinity matrix (New England Biolabs, The NEB Transcript, 3, 14), or simply to require, for its purification, conditions that affect its biological activity. For these reasons is desirable to have different variants, since each protein to express can represent a particular case. With this purpose, they have been developed stabilizer peptides based on the maltose binding protein of *E. coli* (MalE), which have affinity for the amylose resins (European Patent Application EP 0426787 A1 910515); in the chloramphenicol acetyl transferase enzymes (European Patent Application No. EP 0131363 A1 850116) or in the glutation-S-transferase (European Patent Application No. EP 0293249 A1 88130, of the Amrad Corp., Ltd.) obtainable with matrixes of immobilized substrate; in the protein A of *Staphylococcus aureus*, according to the patent application PCT WO 9109946 A1 910711; and in the 12.5 kDa subunity of the transcarboxylase complex of *Propionibacterium shermanii*, which is biotinilated *in vivo* and permits the purification based on the affinity of the biotin by the avidin (Cress, D., Shultz, J. and Breitlow, S., Promega Notes, 42, 2-7, patent applications No. EP 0472658 A1 920304 or WO 9014431 A1 901129).

Of particular interest results the method described in the European Patent Application EP 0472658 A1 920304 or WO 9014431 A1 901129, developed by Biotechnology Research and Development Corporation, along with the University of Illinois, USA. In this application an expression system is described that uses the lipoic acid binding domain of the dihydrolipoamide acetyl transferase (EC 2.3.1.12), also known as the E2 subunit of the pyruvate dehydrogenase complex of *E. coli*. This domain is modified postranslationally *in vivo* by the addition of a lipoic acid molecule to the nitrogen of one of its lysines (Guest, J.R., Angier, J.S. and Russell, G.C., Ann. N. Y. Acad. Sci., 573, 76-99), which is exploited for the purification and identification fused proteins to it through the use of an antibody that recognizes only lipoylate domains.

This method, however, has of a number of drawbacks. First of all, it is known that the over expression of proteins containing binding domains to the lipoic acid exceeds the capacity of cellular lipoylation, producing as consequence not lipoylates domains (Thousands, J.S. and Guest, J.R., Biochem. J., 245, 869-874; Ali, S.T. and Guest, J.R., Biochem. J., 271, 139-145) or octanoilates (Ali, S.T., Moir, A.J., Ashton, P.R. et al. Mol. Microbiol., 4, 943-950; Dardel, F., Packman, L.C. and Perham, R.N., FEBS Lett. 295, 13-16), which can reduce the yield during the purification by immunoaffinity. In second place, there are a group of diseases of a supposed autoimmune origin which have as common factor the presence of antibodies that recognize specifically the lipoic acid in the context of these domains. Among them are the primary biliary cirrhosis, a chronic disease characterized by the inflammation and progressive obstruction of the intrahepatic biliar conduits (Tuailon, N., Andre, C., Briand, J.P. et al., J. Immunol., 148, 445-450); and the hepatitis provoked by the halotane, an anesthetic of wide use that derivatised some proteins by the formation of trifluoroacetyl lysine (Gut, J., Christen, Or., Frey, N. et al, Toxicology, 97, 199-224). The serum of the patients with this disease recognizes said complexes, whose molecular structure is mimicked by the lipoic acid in the context of the dihydrolipoamide acetyl transferases (Gut, J., Christen, Or., Frey, N. et al., Toxicology, 97, 199-224). For this reason is desirable to avoid the presence of the lipoic acid in such peptides if the fusion proteins that contain it constitute vaccine candidates for being used in human.

Disclosure of the Invention.

It is object of the present invention a procedure for the expression to high levels of heterologous proteins as fusion polypeptides in *E. coli*, which is based on the use of a stabilizer sequence derivative from the first 47 amino acids of the P64K antigen of *N. meningitidis* B:4:P1.15 (European Patent application No. 0 474 313 A2) that confers them the capacity of being expressed as inclusion bodies. Said sequence, though presents homology with part of the lipoic acid binding domain of the dihydrolipoamide acetyl transferases, it has been genetically manipulated to eliminate the possibility of modification for itself and presents the advantage of being lowly immunogenic. This procedure also includes the use of a monoclonal antibody that specifically recognizes the mentioned stabilizer, permitting the immunodetection of any protein fused to the same.

Particularly, in the present invention, a recombinant plasmid as an expression vector is used which carries said sequence under the control of the tryptophan promoter (ptrip) of *E. coli*, followed by restriction sites *Xba*I, *Eco*RV and *Bam*HI. These permit the in frame cloning of DNA fragments encoding for polypeptides of interest. This vector also includes a terminator of the transcription of the gene 32 of bacteriophage T4 and a resistance gene to ampicillin as selection marker.

This procedure makes possible also the inclusion of the fusion polypeptide obtained in vaccine preparations destined to be used in humans; and the nature of the stabilizer peptide employed permits the generation of an protective immune response against the foreign protein or the multiepitopic peptide bound to it.

Constitute a novelty of the present invention the genetic manipulation and the use of an homologous stabilizer peptide to part of the lipoic acid binding domain of the dihydrolipoamide acetyl transferases, for the production of fusion proteins by the recombinant DNA technology in *E. coli*. Particularly, constitute novelties of the present invention the use, with the previous objective, of a stabilizer peptide derivative of the first 47 amino acids of the P64K antigen of *N. meningitidis* B:4:P1.15 (European Patent application No. 0 474 313 A2), and a monoclonal antibody that specifically recognizes the stabilizer.

EXAMPLES:

EXAMPLE 1:

The LpdA antigen of *N. meningitidis* (P64K, LpdA) is a protein of 594 amino acids that belongs to the family of the dihydrolipoamide deshydrogenases (EC 1.8.1.4) and specifically, to a new subgroup within them, characterized by possessing a lipoic acid binding domain, analogous to the one present in the dihydrolipoamide acetyltransferases, in its N-terminal portion (Kruger, N., Oppermann, F. B., Lorenzl, H. and Steinbüchel, A., J. Bacteriol., 176, 3614-3630, 1994; Hein, S. and Steinbüchel, A., J. Bacteriol., 176, 4394-4408, 1994). The LpdA protein has been cloned and over expressed in *E. coli*, with the addition of 5 amino acids (MLDKR) in its N-terminal end (European Patent application No. 0 474 313 A2; Figure 1). Although the denominations LpdA and P64K are equivalent, the name P64K for referring to the recombinant protein will be used.

In order to determine the immunogenicity of different fragments from said antigen and to analyze the possibility of using the less immunogenic as stabilizer peptide, the epitopes for B cells present in P64K were located through the evaluation of the reactivity of a polyclonal serum anti-P64k against synthetic peptides.

With this aim, the P64K protein was purified (European Patent application No. 0 474 313 A2) through hydrofobicity chromatography of in Butyl-TSK and gel-filtration; and it was denatured by precipitation with trichloroacetic acid (TCA), neutralizing them with NaOH and balancing in phosphate tampon by gel-filtration chromatography. This preparation was used to immunize 30 mice Balb/c by subcutaneous route with doses of 20 µg adyuvated to 2 µg of aluminium hydroxide (day 0), which were then boosted with the same antigen 7 and 21 days later. Sera were collected 28 days after the first extraction. The sera obtained were combined, and the resulting mixture was alicuoted and stored at -20°C.

Furthermore, 59 peptides of 20 amino acids (a.a.) each covering the entire sequence of the recombinant protein and overlapped by 10 a.a., were synthesized using a commercial kit for the synthesis in solid phase (Multipin Peptide Synthesis System, Chairon Mimotope Pty., Ltd., USA) in 96 wells- plates format and following the instructions given by the manufacturer. These were subsequently numbered from N-terminal end of the protein. The reactivity of the serum antiP64k against these peptides was determined using a dilution 1:2000 of the same, and the format of immunoassay used was the same

as one recommended by the manufacturer of the previous commercial kit.

The results are shown in the Figure 2, in which absorbance values for each peptide are represented. It is evident that the first 110 amino acids (represented by the peptides 1 to the 11) form a poorly immunogenic segment in spite of the denaturation of the immunogen, which can even expose cryptic epitopes. This segment includes essentially the lipoic acid binding domain and the spacer region rich in Proline and Alanine that link it to the rest of the protein. This result demonstrates that the stabilizer peptide (or derivative fragments from it) can be used advantageously as stabilizer peptides, due to the small influence that would have on the immunogenicity of the polypeptides to which is fused. This advantage is especially important if the fusion polypeptide constitutes a vaccine candidate.

EXAMPLE 2:

In order to express different heterologous proteins in *E. coli* through their fusion to the lipoic acid binding domain of the P64K antigen of *N. meningitidis* B:4:P1.15, the expression vector pM-83 was constructed, in which the sequence codifying for a stabilizer peptide, derived from the first 47 amino acid of said protein was introduced (SEQUENCE IDENTIFICATION NUMBER: 1). This sequence is cloned under the control of the tryptophan promoter of *E. coli*, including the terminator of the bacteriophage T4 as signal for the transcription termination, and the ampicillin resistance gene as the selection marker.

To obtain the PM-83 expression vector, the stabilizer peptide was first amplified using the Polymerase Chain Reaction (PCR) (Randall, K. et al., Science, 42394, 487-491, 1988) from the plasmid pM-6, which carries the nucleotide sequence codifying for the P64K antigen (European Patent application No. 0 474 313 A2, Figure 1). For this purpose, the oligonucleotide primers 1573 and 1575 were used, which introduce NcoI and XbaI restriction sites in the amplified DNA fragment that correspond with the amino and carboxyl terminal ends of the stabilizer codified by it:

NcoI

1573: 5' TTCCATGGTAGATAAAAG 3' (SEQUENCE IDENTIFICATION NUMBER: 2)

XbaI

1575: 5' TTTCTAGATCCAAAGTAA 3' (SEQUENCE IDENTIFICATION NUMBER: 3)

The amino acid sequence codified by the resultant stabilizer is shown in Figure 3 (SEQUENCE IDENTIFICATION NUMBER: 6). The introduction of the restriction site NcoI changes Leucine 2 for Valine; and the primer 1575 eliminates the sequence ETD (position 45-47), introducing in its place the sequence DLE. In this way the binding Lysine of the lipoic acid (position 48) does not form part of the stabilizer, and the vicinity of it, which is highly conserved in these domains (Russell, G.C., Guest, J.R., Biochim. Biophys. Record, 1076, 225-232, 1991) is altered. All this guarantees the elimination of the possibilities of postranslational lipoylation of the fusion proteins that contain these domains, and the generation, during the immunization with these proteins, of auto antibodies of similar specificity to those presents in the patients of primary biliary cirrhosis (Tuailon, N., Andre, C., Briand, J.P. et al., J. Immunol., 148, 445-450).

Plasmid pM-83 was constructed through the cloning of this fragment (SEQUENCE IDENTIFICATION NUMBER: 5) previously digested XbaI/NcoI in the plasmid pILM-29 (Guillén, G., Loyal, M., Alvarez, A. et al., Acta Biotechnológica, 15, 97-106, 1995). The pILM29 plasmid contains the gene for the protein Opc (5c) of *N. meningitidis* fused to a stabilizer peptide consistent in the first 58 amino acids of the human IL-2, so that such cloning removes the fragment of IL-2 and fuses the Opc to the stabilizer of the P64K protein (Figure 4). From the resultant plasmid, designated pM-80, the *opc* gene was excised using the enzymes XbaI and BamHI, and in its place was cloned an adapter formed by the hybridization of the oligonucleotides 1576 and 1577, which introduce restriction sites XbaI, EcoRV and BamHI in the extreme 3' of the stabilizer fragment:

1576 5' CTAGATTGATATCAG 3' (SEQUENCE IDENTIFICATION NUMBER: 7)
 1577 3' TAAACTATAGTCCTAG 5' (SEQUENCE IDENTIFICATION NUMBER: 8)

This plasmid was designated pM-83 (Figure 4). The insertion of all the DNA fragments and oligonucleotides, as well as the maintenance of the correct reading frame, were verified by DNA sequence according to Sanger, F. et al., (PNAS, USA, 74: 54631977).

EXAMPLE 3:

It is important that the stabilizer does not contain regions of high homology with human proteins if the resulting fusion protein is a vaccine candidate. The determination of the similarity of the stabilizer peptide of the pM-83 (EXAMPLE 2) with human proteins was

accomplished through a search of homology in the data bases EMBL Data Library v.38 (Curl, C.M., Fuchs, R., Higgins, D.G. et al., Nucl. Acids Beast. 21, 2967-2971, 1993) of nucleotide sequences, and SWISS-PROT v.38 (Bairoch, A. and Boeckmann, B., Nucl. Acids Beast. 21, 3093-3096, 1993) of amino acid sequences; both March versions of 1994. For this search two of the programs BLAST were used (Altschul, S.F., Gish, W., Miller, W., Myers, And.W. and Lipman, D.J., J. Mol. Biol., 215:403-410, 1990): BLASTP, that compares one amino acid sequence against a base of protein sequences (in this case SWISS-PROT) and TBLASTN, that compares an amino acid sequence against all the translations in both directions and in all the reading frames of a base of nucleotide sequences, as in this case the EMBL Data Library; in both cases it was used a valorization matrix PAM120 [Dayhoff, M. O., Schwartz, R.M. and Orcutt, B.B., in: Dayhoff, M.Or. (of.), Atlas of Protein Sequence and Structure, 5, supl.3, 345-352, Natn. Biomed. Beast. Found., Washington, 1978].

The result can be observed in Figures 5 and 6, in which the sheets of the respective results of the BLASTP and the TBLASTN are shown (homologous sequences of prokaryotes or inferior eukaryotes have been omitted for a better understanding). It is obvious that no human protein or from any other mammals presents meaningful similarities with the stabilizer derived from the P64K; since the homologies detected by both algorithms (in the human and rat piruvate kinases; and the C-terminal end of the human and canine mucines) present a highest casual occurrence probability (as a comparison point, the same probability, for the case of the dihydrolipoamide acetyltransferase of *Azotobacter vinelandii*, it is of 3.7×10^{-5}).

Of all of the above mentioned it can be concluded that the use of said stabilizer in vaccine candidates is absolutely sure.

EXAMPLE 4:

The capacity of the present stabilizer in the pM-83 of permitting the intracellular synthesis at high levels and in the form of inclusion bodies was evaluated, comparing the expression of several proteins fused to the first 22 or 58 amino acids of the human Interleukine-2 (IL-2), a fusion peptide very used with this end, or fused to the first 47 a.a. of the P64K antigen modified according to is described in the EXAMPLE 2.

For this purpose the genes codifying for the outer membrane proteins of *N. meningitidis* B:4:P1.15 PorA and Opc were cloned into

the vectors pFP15 (hIL2-58; European Patent No. 416 673 B1) or pM-83 (P64K-47); and in the vectors pISL31 (hIL2-22, Castellanos-Sierra, L.R., Hardy, E., Ubieta, R., et al., paper submitted) or pM-83, the genes codifying for a multiepitopic polypeptide (MEP) that includes immunogenic regions of several isolates of the Human Immunodeficiency Virus, HIV. The resultant expression plasmids are: pILM-28 (IL2-58 PorA; Guillén, G., Alvarez, A., Lion, L., et al., 494-498 in: Conde-González, C. J., Morse, S., Rice, P. et al. (eds.), Pathobiology and Immunobiology of *Neisseriaceae*, Instituto de Salud Pública Nacional, Cuernavaca, Mexico, 1994), pM-82 (P64K-47 PorA; Niebla, O., Alvarez, A., González, S. et al., 85-86 in: Evans, J.S., Yost, S. and Maiden, M.C.J. et al. (eds.), *Neisseria* 94: Proceedings of the IX International Pathogenic *Neisseria* Conference, Winchester, England, 1994), pILM-29 (IL2-58 Opc; Guillén, G., Leal, M., Alvarez, A. et al., *Acta Biotecnológica*, 15, 97-106, 1995), pM-80 (EXAMPLE 2, Figure 4), pTAB4 (IL2-22 + MEP) and pTAB9 (P64K-47 MEP).

The TAB4 and TAB9 proteins are multiepitopic polypeptides (MEP) that include several copies of the central part of the variable region 3 (V3) of the gp120 protein of the HIV-1. For the construction of these MEP, 15 central amino acids of the region V3 of the following isolates were selected:

LR150: SRGIRIGPGRAILAT (SEQUENCE IDENTIFICATION NUMBER: 9)

JY1: RQSTPIGLGQALYTT (SEQUENCE IDENTIFICATION NUMBER: 10)

RF: RKSITKGPGRVIYAT (SEQUENCE IDENTIFICATION NUMBER: 11)

MN: RKRIHIGPGRAFYTT (SEQUENCE IDENTIFICATION NUMBER: 12)

BRVA: RKRITMGPGRVYYTT (SEQUENCE IDENTIFICATION NUMBER: 13)

IIIB: SIRIQRGPGRAFVTI (SEQUENCE IDENTIFICATION NUMBER: 14)

These regions are bound by a spacer peptide of five amino acids, of sequence AGGGA (SEQUENCE IDENTIFICATION NUMBER: 17).

To achieve this, the DNA sequence codifying for the V3 epitopes bound by the spacer peptide was obtained by chemical synthesis (SEQUENCE IDENTIFICATION NUMBER: 21) and was cloned under the control of the tryptophan promoter, fused to the first 22 amino acids of the human IL-2 (Figure 7). From the resultant plasmid, designated pTAB3, a fragment containing the gene for the MEP, the tryptophan promoter and the T4 terminator was excised by digestion with the enzymes *ScaI* and *HindIII*, and is cloned into pUC19 (Yanisch-Perron, C. et al., 1985, *Gene* 33, 103-119) to obtain the pTAB4 (Figure 7). Finally, the pTAB9 was constructed eliminating the sequence codifying for the stabilizer derived from the human IL-2 by digestion with the enzymes *NcoI* and *XbaI*, and cloning, in its place, a fragment codifying for

the first 47 amino acids of the P64K antigen obtained by polymerase chain reaction (PCR), as is described in the EXAMPLE 2. The sequence of the resultant MEP is shown in Figure 8, and its organization in Figure 9 A.

The host strains of *E. coli* K-12 used for all these plasmids were the W3110 (Hill, C.W., and Hamish, B.W. Proc. Natl. Acad. Sci., 78, 7069, 1981; Jensen, K. F., J. Bacteriol., 175, 3401-3407, 1993) for pILM-28, pILM-29, pM-80 and pM-82; and the W3110 *trpA905*, for pTAB4 and pTAB9. The expression was achieved in all the cases inoculating a culture of 5 mL of LB medium (Sambrook, J., Fritsch, Y. F. and Maniatis, T., Molecular Cloning: To Manual Laboratory, Cold Spring Harbor Laboratory Press, 1989, New York, USA) with ampicillin (Ap) to 50 µg/mL and tryptophan (W) to 100 µg/mL, which was grown 12 h at 37°C. Said culture was used to inoculate a culture of 50 mL of LB-Ap (pTAB4 and pTAB9) or a defined medium compound by M9 salts (Miller, J.H., Experiments in Molecular Genetics, Cold Spring Harbor Laboratory Press, 1972, New York, USA), glucose to 1%, casein hydrolyzate to 1%, CaCl₂ 0.1 mM, MgCl₂ 1mM and Ap to 50 ug/mL (pILM-28, pILM-29, pM-80, pM-82), those which were grown 12 h to 37°C and 250 r.p.m. After this time, total protein samples were taken and analyzed by denatured polyacrilamide gel electrophoresis (SDS-PAGE, Laemmli, O. K., Nature, 277, 680, 1970s) and staining with Coomassie Brilliant Blue R-250. The expression percent was analyzed in a densiometre of laser Bromma-LKB. Their cellular location was determined by lysing the cells through treatment combined with lysozyme and ultrasound, after something then the soluble proteins were separated from the insoluble ones by centrifugation. The insolubility of the protein was used as criterion to assume its expression as inclusion bodies, since other conditions under which they can exhibit said behavior (association to membranes or to the peptide glycan) are unlikely in this case.

A summary of the results can be seen in the Figure 10 A. In all the cases the expression under the stabilizer derived from the P64K is comparable to the expression obtained when fused to peptides of the IL-2 concerning the relationship of heterologous protein: total cellular protein (see Figure 10 B for the case of the MEP), which confirms the capacity of the pM-83 to be used as vector for the expression of fusion peptides. It is worth nothing that these polypeptides are to hard to express in *E. coli* if they are not fused, either by their small size and sensibility to proteases of the host, as the MEP, or by their toxicity in the case of the protein PorA and the bacterial porins in general (Carbonetti, N.H. and Sparling, P.F.; Proc. Natl. Acad. Sci. U.S.A., 84, 9084-9088). In all the cases the

product was obtained as inclusion bodies, as is exemplified for the pTAB9 (Figure 10 C).

In conclusion, it is possible to outline that the use of the stabilizer derivative from the first 47 amino acids of the P64K antigen of *N. meningitidis* (P64K-47) results in an efficiency of expression of heterologous proteins as inclusion bodies, comparable to that of other systems (European patent applications No. 0 416 673 A2 and No. 229 998, Hoechst AG; European patent No. 0 416 673 B1; Castellanos-Sierra, L.R., Hardy, E., Ubieta, R., et al., manuscript submitted), with the additional benefit for the product of being used directly (i.e., without separating it from the stabilizer) due to the absence of meaningful homology with antigens of human origin.

EXAMPLE 5:

The availability of a ligand that recognizes specifically the stabilizer (e.g. an antibody, an enzymatic cofactor, etc.) is a desirable characteristic in any expression system of recombinant proteins. This is due to that the foregoing can permit, for instance, the design of efficient plans of affinity purification if said ligand is immobilize in a chromatographic resin; and even - in the case of the antibodies - the follow-up of the intermediate steps of the purification through immunologic techniques, independently of the identity of the expressed heterologous protein.

Such an objective was reached immunizing mice with the protein TAB13 (SEQUENCE IDENTIFICATION NO.: 20) in order to obtain monoclonal antibodies (MAb) against this stabilizer. TAB13 it is a MEP derived from the TAB9 which is different from the former by the presence of two additional V3 consensus regions (Figure 9 B):

-C6: TSITIGPGQVFYRTG (SEQUENCE IDENTIFICATION NO.: 15)

-C8: RQRTSIGQGQALYTT (SEQUENCE IDENTIFICATION NO.: 16)

This MEP was expressed (EXAMPLE 4) and purified (EXAMPLE 6) in an analogous way to that described for the TAB4 and TAB9.

Then, mice Balb/c were immunized by subcutaneous route with 3 doses of 20 μ g of TAB13 adyuvated in aluminium hydroxide at a 15 days-interval. The animal were boosted by intraperitoneal route with 20 μ g of the same antigen in buffer phosphate, 20 days after the last dose. The splecnocytes were fused with the myeloma X63 Ag8 653 and the resultant hybridomas were isolated and tested according to established methods (Gavilondo, J. V. (ed.), Monoclonal Antibodies: Theory and Practical, Elfos Scientiae, 1995, The Havana, Cuba).

The reactivity of the antibodies secreted by the isolated hybridomas was evaluated by ELISA, coating the plates with the MEP TAB13, the P64K protein or synthetic peptides representing the different V3 regions present in TAB13. In total 18 positive clones were obtained, one of which, designated 448/30/7, recognized TAB13 as well as 64K, but none of the peptides from the gp120.

The specificity of this MAb by the stabilizer peptide of the pM-83 and the possibility of its use for the immunologic detection of proteins that contain it, was determined by Western blotting, using different samples, heterologous proteins fused to the stabilizer derived from P64K (P64K-47), or the same fused protein or to the first 58 amino acids of the IL-2 (IL2-58). To do this, the *E. coli* strain MM294 was transformed (Sambrook, J., Fritsch, E. F. and Maniatis, T., Molecular Cloning: To Manual Laboratory, 1989, Cold Spring Harbor Laboratory Press, New York, USA) with the following plasmids: pILM-28 (IL2-58 + *porA*), pM-82 (P64K-47 + *porA*), pTAB13 (P64K-47 + MEP), pM-6 (P64K) and pFP15 (IL-2). The expression plasmid pM-134 was also used, which contains the first 120 amino acids of the P64K, which includes the binding domain to the lipoic acid under the control of the same regulatory signals as in the previous plasmids. This segment was amplified by PCR using the primer 1573 (SEQUENCE IDENTIFICATION NO.: 2) and 2192 (SEQUENCE IDENTIFICATION NO.: 4); it was digested with the enzymes NcoI and BamHI, and was cloned in the plasmid pFP15 (see EXAMPLE 4) digested identically. The expression of these transformants was achieved in the growth conditions specified in the EXAMPLE 4 for the pTAB4 and the pTAB9.

The results obtained are represented in Figure 11. As can be appreciated, MAb 448/30/7 recognizes a probably linear epitope within the stabilizer P64K-47, due to its reactivity with the samples of the plasmids pM-6, pM-82, pTAB13 and pM134 in spite of all these proteins be antigenically different. This experiment demonstrates that in no case this reactivity is due to the protein fused to the stabilizer (e.g. plasmids pILM-28 and pM-82: both carry the gene *porA* under different stabilizer) which evidences the specificity of recognition of this MAb.

In conclusion, the expression system formed by the stabilizer P64K-47, the plasmids that contain it and MAb 448/30/7 permit the efficient synthesis and in the form of inclusion bodies of a great variety of proteins, and their detection without the previous

availability of immunologic probes against each polypeptide to express.

EXAMPLE 6:

The absence of deleterious effects on the immune response against the polypeptide fused to the stabilizer is an important factor to take into account upon selecting an expression system for vaccine candidates. One of the advantages of the expression system based on the stabilizer P64K-47 is precisely its decreased immunogenicity (EXAMPLE 1) which guarantees the foregoing. Nevertheless, the influence of the stabilizer P64K-47 in the immune response against the fused protein was evaluated qualitatively through the comparison of the antibodies response against the different peptides of the V3 region present in the MEP TAB4 (IL2-22) and TAB9 (P64K-47).

For the expression and the purification of TAB4 and TAB9, the biomass of the strain W3110 *trpA905* + pTAB4 and W3110 *trpA905* + pTAB9 was obtained as described in the EXAMPLE 4. This biomass was broken combining the treatment with lysozyme and with ultrasound in fluoride presence of phenyl methyl sulfonyl (PMSF) and the non-ionic detergent Tritón-X-100; the inclusion bodies were obtained by differential centrifugation, and the MEP were partially purified and solubilized by two successive wash cycles of the inclusion bodies with caotrophic agents and detergents (TAB4: 1. Urea 4 M Tritón-X-100 1%, 2. Urea 8 M. TAB9: 1. Urea 8 M Tritón-X-100 1%, 2. guanidium chloride 6 M). The supernatants obtained were finally purified through a gradient from 20 to 80% of acetonitrilo in a column C4 VYDAC of high performance liquid chromatography (HPLC), being achieved 90% of purity approximately.

The purified recombinant proteins were adyuvated in gel of aluminium hydroxide using a relationship of 60 mg of adyuvant per mg of protein. These preparations were used to immunize 5 groups of rabbits by subcutaneous route with 200 µg/dose. The immune response was evaluated by ELISA, using polystyrene plates of 96 wells (High binding, Costar, USA), well coated with the MEP used for the immunization, or with peptides corresponding to each one of the V3 regions present on it. The titers were calculated as the maximum dilution of each serum with an absorbance value of twice higher than that of a mixture of pre immune sera. All the sera were analyzed by duplicate.

The values obtained (Figure 12) show that the titers against the V3 regions are similar between the varying IL2-22 + MEP (TAB4) and P64K-47 + MEP (TAB9). Though the recognition frequency of the peptides is slightly greater for the TAB9, this difference is not meaningful statistically ($p < 0.05$). In conclusion, the immunogenicity of the heterologous protein is affected by the stabilizer P64K-47 in a minimal way, and comparable to other expression systems currently in use.

Description of the Figures:

Figure 1: Nucleotide sequence of the gene *lpdA* gene codifying for P64K. It is shown in *italic* the sequence added in the plasmid pM-6 (European Patent application No. 0 474 313 A2), absent originally in the gene *lpdA*.

Figure 2: Reactivity of the polyclonal serum of mouse against peptides of the P64K. A minimal value of 0.4 optical density units to consider the result as positive was chosen.

Figure 3: Amino acid sequence of the stabilizer, deduced of the DNA sequence amplified by PCR from plasmid pM-6. The underlined sequences correspond to the oligonucleotide primers.

Figure 4: Strategy for the construction of plasmid pM-83.

Figure 5: Results of the search of homology between the sequences of the stabilizer ('Query') and those present in the SWISS-PROT ('Sbjct') base, using the BLASTP program. The corresponding income for human proteins or for mammals proteins are only shown. P(N) represents the probability of finding N equal alignments within a base composed of random sequences; the significance of the homology diminishes with the value of P(N). Identical residues are represented with their codes of one letter; the conservatives substitutions with a '+', and the differences are not indicated.

Figure 6: Results of the search of homology between the sequences of the stabilizer ('Query') and all the possible translations of the sequences of the EMBL Data Library ('Sbjct'), using the program TBLASTN. The corresponding income to human proteins or mammal proteins are only shown. P(N) represents the probability of finding N equal alignments within a base composed of random sequences; the significance of the homology diminishes with the value of P(N). Identical residues are represented with their code of one letter; the conservative substitutions with a '+', and the differences are not indicated.

Figure 7: Strategy for the construction of plasmids pTAB4 and pTAB9.

Figure 8: Nucleotide and amino acid sequences of the MEP TAB9.

Figure 9: A: General structure of the MEP TAB4 and TAB9. B: General structure of the MEP TAB13.

Figure 10: Comparison of the expression of the genes *porA*, *opc* and the MEP under stabilizer derivatives from the human IL-2 or from the first 47 amino acids of the P64K antigen.

A: Comparative table. hIL2-58 it is referred to the first 58 amino acids of the human IL-2, hIL2-22 to the first 22, and P64K-47 to stabilizer derivative from the first 47 amino acids of the P64K antigen.

B: Comparative analysis by SDS-PAGE of the expression of the MEP in the plasmids TAB4 and TAB9. Lane A: Molecular weight markers; B: Total proteins of the strain W3110 *trpA905*; C: Total proteins of W3110 *trpA905* + pTAB4; D: Purified TAB4; E: Total proteins of W3110 *trpA905* pTAB9; F: Purified TAB9.

C: Expression of TAB9 in inclusion bodies. A: Soluble proteins of the sample. B: Insoluble proteins or of membrane.

Figure 11: Western blotting using MAb 448/30/7 with total protein samples of *E. coli* MM294 transformed with: 1: Negative control, 2: pM-6 (P64K), 3: pM-82 (P64K-47 + *porA*), 4: pTAB13 (P64K-47 + MEP), 5: pFP15 (IL-2), 6: pM-134 (P64K-120), 7: pILM-28 (IL2-58 + *porA*). The molecular weight markers are indicated on the left.

Figure 12: Reciprocal of the titter value by ELISA of the rabbits immunized with TAB4 and TAB9. MG: Geometric mean of the reciprocal of the titters anti V3; R: Percent of reactivity with the V3 peptides.

CLAIMS:

1. Fusion protein which contains a stabilizer peptide derived from the first 47 amino acids of the N-terminal end of the P64K antigen of *Neisseria meningitidis* B:4:P1.15 fused to an heterologous protein.
2. Fusion protein according to claim 1 wherein the heterologous protein is an outer membrane protein of *Neisseria meningitidis*.
3. Fusion protein according to claim 2 wherein the heterologous protein is the Opc(5c) protein of *Neisseria meningitidis* or the PorA protein of *Neisseria meningitidis*.
4. Fusion protein according to claim 1 wherein the heterologous protein are multiepitopic polypeptides which include several copies of the central part of the variable region 3 (V3) from the gp 120 protein from HIV-1.
5. Fusion protein according to claim 4 wherein the multiepitopic polypeptides are the polypeptides TAB4 and/or TAB9.
6. Method for producing heterologous proteins as fusion polypeptides in *E. coli* wherein a peptide derived from the first 47 amino acids of the N-terminal end of the P64K antigen of *Neisseria meningitidis* B:4:P1.15 is used as stabilizer for the expression of said heterologous protein and a monoclonal antibody specific for the stabilizer is used for the immunodetection of any protein fused to it.
7. Method according to claim 6 wherein the amino acid sequence of the stabilizer peptide corresponds essentially to the sequence of Id. Seq. No. 6.

10 20 30 40 47

MVDKRMALVE LKVPDIGGHE NVDIIAVEVN VGDTIAVDDT LITLDLE
8. Method according claim 6 wherein the monoclonal antibody used for the purification of the fusion protein is designated as 448/30/7.
9. Method according to claim 6 wherein the expressed heterologous protein is any protein that could be employed as immunogen in a vaccine preparation.
10. Method according to claim 6 wherein the expressed heterologous protein are the multiepitopic polypeptides TAB4 and/or TAB9, or the outer membrane proteins Opc(5c) or PorA of *Neisseria meningitidis*.
11. Monoclonal antibody 448/30/7 which is specific for the stabilizer peptide derived from the first 47 amino acids of the N-terminal end of the P64K antigen of *Neisseria meningitidis* B:4:P1.15 and it is used for the immunodetection and purification of any protein fused to said stabilizer peptide.
12. Expression vector of fusion proteins in *E. coli* which contains a sequence encoding for a stabilizer peptide derived from the first 47 amino acids of the N-terminal end of the P64K antigen of *Neisseria meningitidis* B:4:P1.15 under the control of the tryptophan promoter of *E. coli* followed by restriction sites XbaI, EcoRV and BamHI for the cloning in frame of DNA fragments encoding for polypeptides of interest and the phage T4 terminator as the

transcription termination signal, as well as a resistance gene as selection marker.

13. Expression vector according to claim 12 for the cloning in frame of DNA fragments encoding for outer membrane proteins of *Neisseria meningitidis*.

14. Expression vectors according to claim 13 denominated pM-80 pM-82.

15. Expression vectors according to claim 12 for the cloning in frame of DNA fragments encoding for outer membrane proteins of *Neisseria meningitidis*.

13. Expression vector according to claim 12 for the cloning in frame of DNA fragments encoding for outer membrane protein of meningitidis.

14. Expression vector according to claim 12 for the cloning in frame of DNA fragments encoding for the V3 region 3 (V3) of HIV-1.

14. Expression vectors according to claim 13 denominated pM-80 for meningitidis.

15. Expression vector according to claim 12 for the cloning in frame of DNA fragments encoding for multiepitopic polypeptide which includes copies of the central part of the variable region 3 (V3) belonging to gp 120 protein from HIV-1.

16. Transformation vectors according to claim 15 denominated pTAB4 and pTAB5 for the transformation of *Escherichia coli* cells.

16. Expression vectors according to claim 15 denominated pTAB4 and pTAB9.

16. Expression vectors according to claim 15, belonging to gp120 and pTAB9.

17. Recombinant strain of *E. coli* which results of the transformation of any *E. coli* K12 strain with any of the expression vectors of claims 12 to 16.

18. The fusion protein of claims 1 to 8 in vaccine for animals.

19. The fusion protein of claims 1 to 8 in any of the

17. Recombinant strain of any *E. coli* K12 strain with any of claims 12 to 16.

18. Use of the fusion protein of claims 1 to 8 in vaccine preparations to be used in human or animals.

19. Preparation which contains a fusion protein of any of the claims as an adjuvant.

18. Use of the fusion protein of claims 12 to 16.
19. Preparations to be used in human or animals.
20. Vaccine preparation which contains a fusion protein of any of the claims 1 to 8 as well as a suitable adjuvant.

Abstract

The present invention relates to biotechnology and genetic engineering, particularly the expression of proteins of viral origin in microorganisms through their fusion, by applying the recombinant DNA technology, to bacterial peptides. The present invention provides an efficient process for the expression in *Escherichia coli* of heterologous proteins as fusion polypeptides with a view to obtaining them with a high degree of purity, in commercially useful amounts, and in an appropriate form for their inclusion in vaccine preparations intended to human use. To this effect, what is essentially used is a stabilizing sequence derived from the first 47 amino acids of the antigen P64k of *Neisseria meningitidis* B:4 :P1.15. In particular, use is made of a recombinant plasmid containing said sequence, under the control of the tryptophane promotor of *E. coli* and of the terminator of the transcription of the phage T4, including restriction sites which provide for the cloning in phase of DNA fragments coding for polypeptides of interest. The process of the invention is applicable to the pharmaceutical industry, for the development of diagnostic systems, vaccine preparations, and in any situation where it is required to obtain high amounts of heterologous proteins as fusion polypeptides in *E. coli*.

FIG. 1

10	20	30	40	50	60	70
ATGCTAGATA	AAAGAATGGC	TTTAGTTGAA	TTGAAAGTGC	CCGACATTGG	CGGACACGAA	AATGTAGATA
80	90	100	110	120	130	140
TTATCGCGGT	TGAAGTAAAC	GTGGGCGACA	CTATTGCTGT	GGACGATACC	CTGATTACTT	TGGAAACCGA
150	160	170	180	190	200	210
TAAAGCGACT	ATGGACGTAC	CTGCTGAAGT	TGCAGGCGTA	GTCAAAGAAG	TTAAAGTTAA	AGTCGGCGAC
220	230	240	250	260	270	280
AAAATCTCTG	AAGGTGGTTT	GATTGTCTGC	GTTGAAGCTG	AAGGCACGGC	AGCCGCTCCT	AAAAGCCGAAG
290	300	310	320	330	340	350
CGGCTGCCGC	CCCGGCGCAA	GAAGCCCCTA	AAGCTGCCGC	TCCTGCTCCG	CAAGCCGCGC	AATTCGGCGG
360	370	380	390	400	410	420
TTCTGCCGAT	GCCGAGTACG	ACGTGGTCGT	ATTGGGTGGC	GGTCCCGGCG	GTTACTCCGC	TGCATTGCCC
430	440	450	460	470	480	490
GCTGCCGATG	AAGGCTTGAA	AGTCGCCATC	GTCGAACGTT	ACAAAACTTT	GGGCGGCGTT	TGCCTGAACG
500	510	520	530	540	550	560
TCGGCTGTAT	CCCTTCCAAA	GCCTTGTTGC	ACAATGCCGC	CGTTATCGAC	GAAGTGGCGC	ACTTGCTGTC
570	580	590	600	610	620	630
CAACGGTATC	AAATACCCCG	AGCCGGAAGT	CGACATCGAT	ATGCTTCGCG	CCTACAAAGA	CGGCGTAGTT
640	650	660	670	680	690	700
TCCCGCCTCA	CGGGCGGTTT	GGCAGGTATG	GCGAAAAGCC	GTAAGTGGGA	CGTTATCCAA	GGCGACGGGC
710	720	730	740	750	760	770
AATTCTTAGA	TCCGCACCAC	TTGGAAGTGT	CGCTGACTGC	CGGCGACGCG	TACGAACAGG	CAGCCCCTAC
780	790	800	810	820	830	840
CGGCGAGAAA	AAAATCGTTG	CCTTCAAAAA	CTGTATCATT	GCAGCAGGCA	GCCGCGTAAC	CAAAGTGCCT
850	860	870	880	890	900	910
TTCATTCCTG	AAGATCCGCA	CATCATCGAT	TCCAGCGGCG	CATTGGCTCT	GAAAGAAGTA	CCGGGCAAAAC
920	930	940	950	960	970	980
TGCTGATTAT	CGGCGGCGGC	ATTATCAGCC	TCGAGATGGG	TACGGTTTAC	AGCACGCTGG	GTTTCGCTTT
990	1000	1010	1020	1030	1040	1050
GGATGTGGTT	GAAATGATGG	ACGGCCTGAT	GCAAGGCGCA	GACCGCGATT	TGGTAAAAAGT	ATGGCAAAAA
1060	1070	1080	1090	1100	1110	1120
CAAAACGAAT	ACCGTTTTGA	CAACATTATG	GTCAACACCA	AAACCGTTGC	AGTTGAGCCG	AAAGAAGACG
1130	1140	1150	1160	1170	1180	1190
GCGTTTACGT	TACCTTTGAA	GGCGCGAACG	CGCCTAAAGA	GCCGCAACGC	TACGATGCCG	TATTGGTTGC
1200	1210	1220	1230	1240	1250	1260
CGCCGGCCGC	GCGCCCAACG	GCAAACTCAT	CAGCGCGGAA	AAAGCAGGCG	TTGCCGTAAC	CGATCGCGGC
1270	1280	1290	1300	1310	1320	1330
TTCATCGAAG	TGGACAAACA	AATGCGTACC	AATGTGCCGC	ACATCTACGC	CATCGGCGAC	ATCGTCGGTC
1340	1350	1360	1370	1380	1390	1400
AGCCGATGTT	GGCGCACAAA	GCCGTTCCAG	AAGGCCACGT	TGCCGCCGAA	AACTGCGCCG	GCCACAAAGC
1410	1420	1430	1440	1450	1460	1470
CTACTTCGAC	GCACGCGTGA	TTCCGGGCGT	TGCCTACACT	TCCCCCGAAG	TGGCGTGGGT	GGGCGAAACC
1480	1490	1500	1510	1520	1530	1540
GAAGTGTCCG	CCAAAGCCTC	CGGCCGCAAA	ATCACCAAAAG	CCAACTTCCC	GTGGGCGGCT	TCCGGCCGTG
1550	1560	1570	1580	1590	1600	1610
CGATTGCCAA	CGGTTGCGAC	AACGGCTTTA	CCAAGCTGAT	TTTTGATGCC	GAAACCGGCC	GCATCATCGG
1620	1630	1640	1650	1660	1670	1680
CGGCGGCATT	GTCGGTCCGA	ACGGTGGCGA	TATGATCGGC	GAAGTCTGCC	TTGCCATCGA	AATGGGCTGC
1690	1700	1710	1720	1730	1740	1750
GACGCGGCAG	ACATCGGCAA	AACCATCCAC	CCGCACCCGA	CCTGGGGCGA	ATCCATCGGT	ATGGCGGGCG
1760	1770	1780	1790	1797		
AAGTGGCATT	GGGTACTTGT	ACCGACCTGC	CTCCGCAAAA	GAAAAAA		

FIG. 2

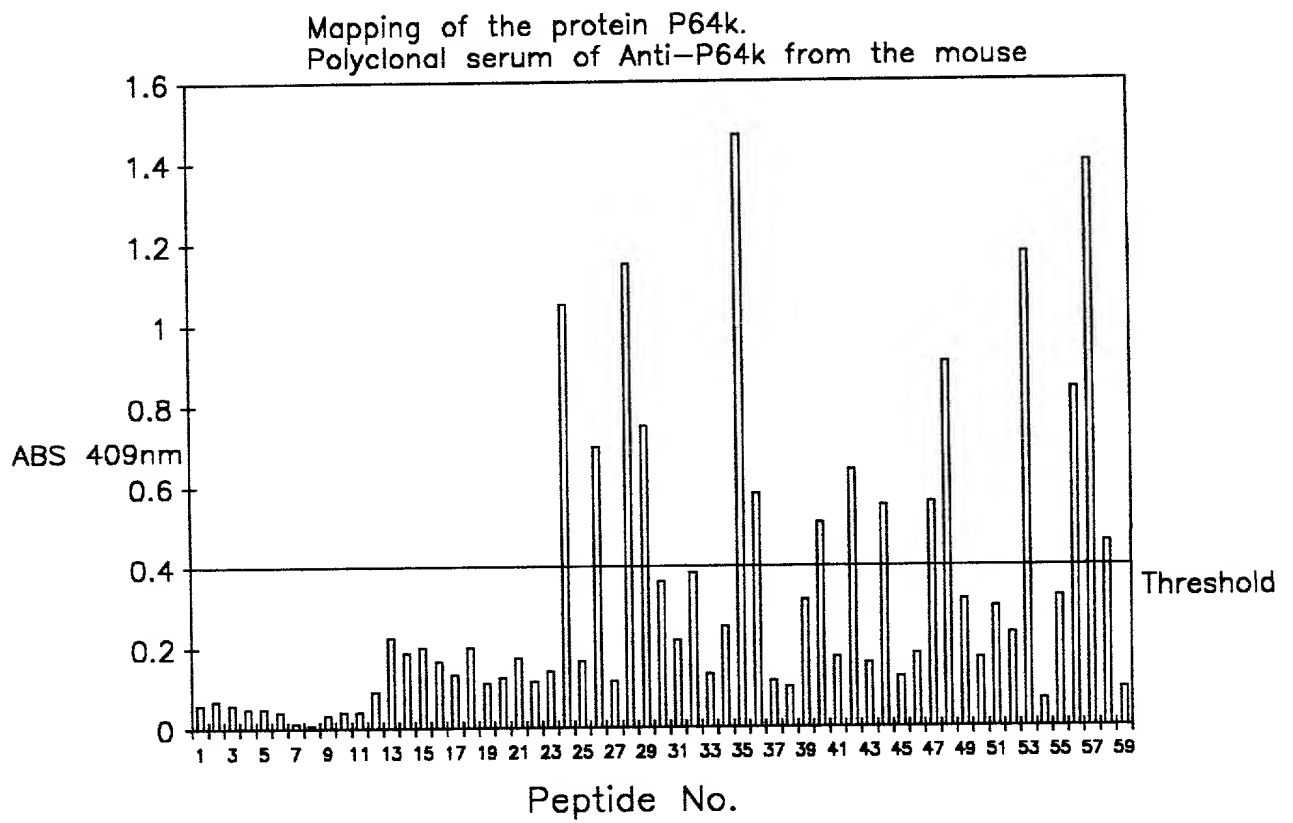


FIG. 3

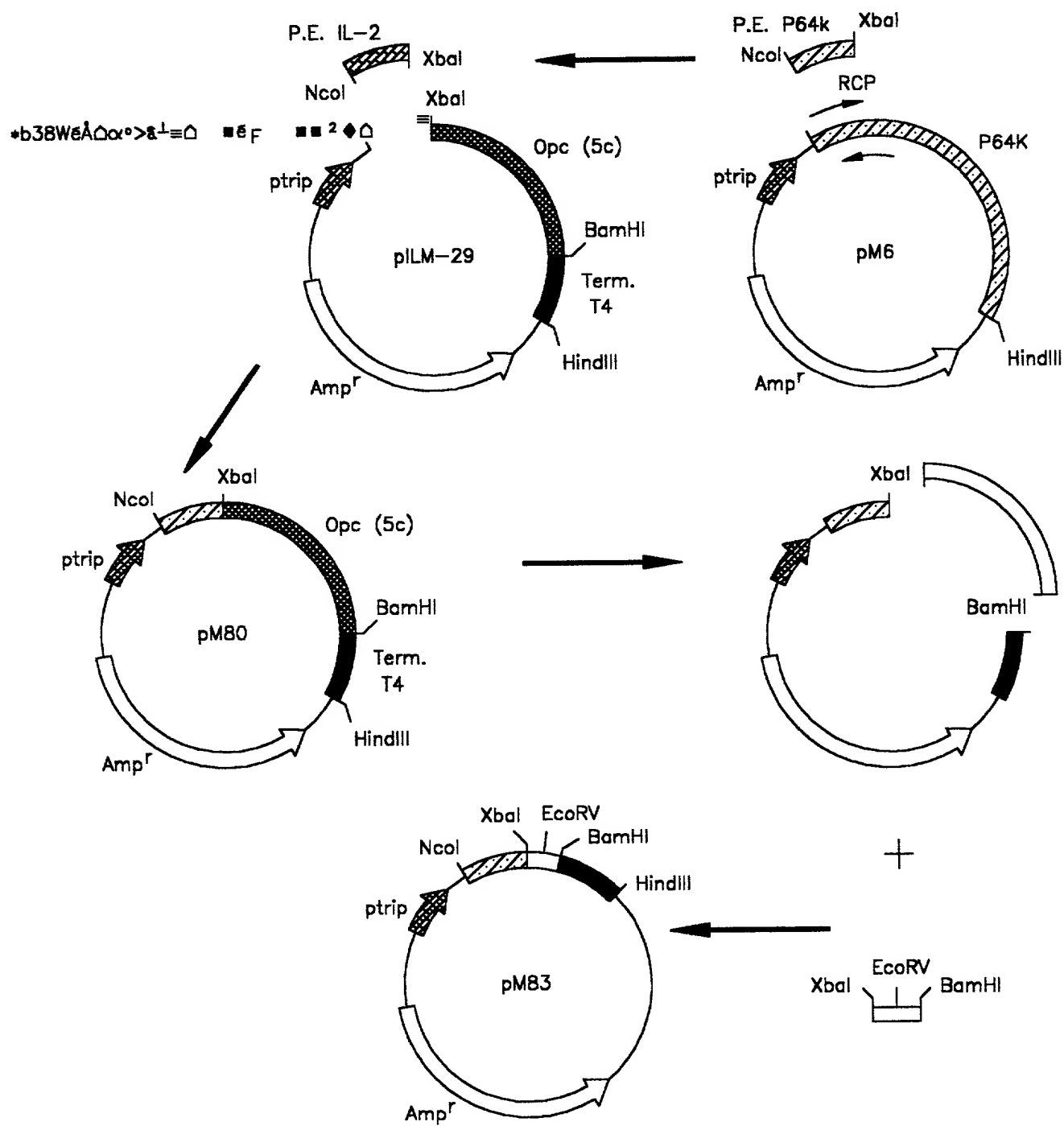
4
5' TTCC

16 25 34 43 52
M V D K R M A L V E L K V P D I G G H
ATG GTA GAT AAA AGA ATG GCT TTA GTT GAA TTG AAA GTG CCC GAC ATT GGC GGA CAC

61 70 79 88 97 106 115
E N V D I I A V E V N V G D T I A V D
GAA AAT GTA GAT ATT ATC GCG GTT GAA GTA AAC GTG GGC GAC ACT ATT GCT GTG GAC

124 133 142
D T L I T L D L E
GAT ACC CTG ATT ACT TTG GAT CTA GAA A 3'

FIG. 4



[illegible]

KPY1_HUMAN PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).
 KPY1_RAT PYRUVATE KINAZE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).
 KPY2_HUMAN PYRUVATE KINAZE, M2 ISOZYME (EC 2.7.1.40).
 KPY2_RAT PYRUVATE KINAZE, M2 ISOZYME (EC 2.7.1.40).

High Score	Smallest Poisson	
	Probability P(N)	N
0.9999	0.0001	1
0.9990	0.0010	1
0.9900	0.0100	1
0.9500	0.0500	1
0.9000	0.1000	1
0.8000	0.2000	1
0.7000	0.3000	1
0.6000	0.4000	1
0.5000	0.5000	1
0.4000	0.6000	1
0.3000	0.7000	1
0.2000	0.8000	1
0.1000	0.9000	1
0.0500	0.9500	1
0.0100	0.9900	1
0.0010	0.9990	1
0.0001	0.9999	1

Query: 29 VNVGDTIAVDDTLITLDDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

Query: 29 VNVGDTIAVDDTLITLDDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

[illegible]

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Poisson Probability P(N)	N
CFMUCIN	Canis familiaris (clone pCTM-A) mucin c-term...	-2	62	0.30	1
HS8671	EST02755 Homo sapiens cDNA clone HFBCA72 sim...	-2	61	0.40	1
>CFMUCIN	Canis familiaris (clone pCTM-A) mucin c-terminus RNA, 3' end. Length = 1733				
Query:	8 LVELKVPDIGGHENVDIIAVEVNVGDTIAVDD 39 L E+ VPD H V+++A E+ +G+++ VDD				
Sbjct:	1015 LREVQVPDRKLHKGVQLLAGELGIGEALQVDD 920				
>HS8671	EST02755 Homo sapiens cDNA clone HFBCA72 similar to Mucin CTM-A. Length = 286				
Query:	8 LVELKVPDIGGHENVDIIAVEVNVGDTIAVDD 39 L E+ VPD HE V++++ E+ VG VDD				
Sbjct:	240 LREVQVPDRKLHEGVQLLSGELGVGKXFQVDD 145				

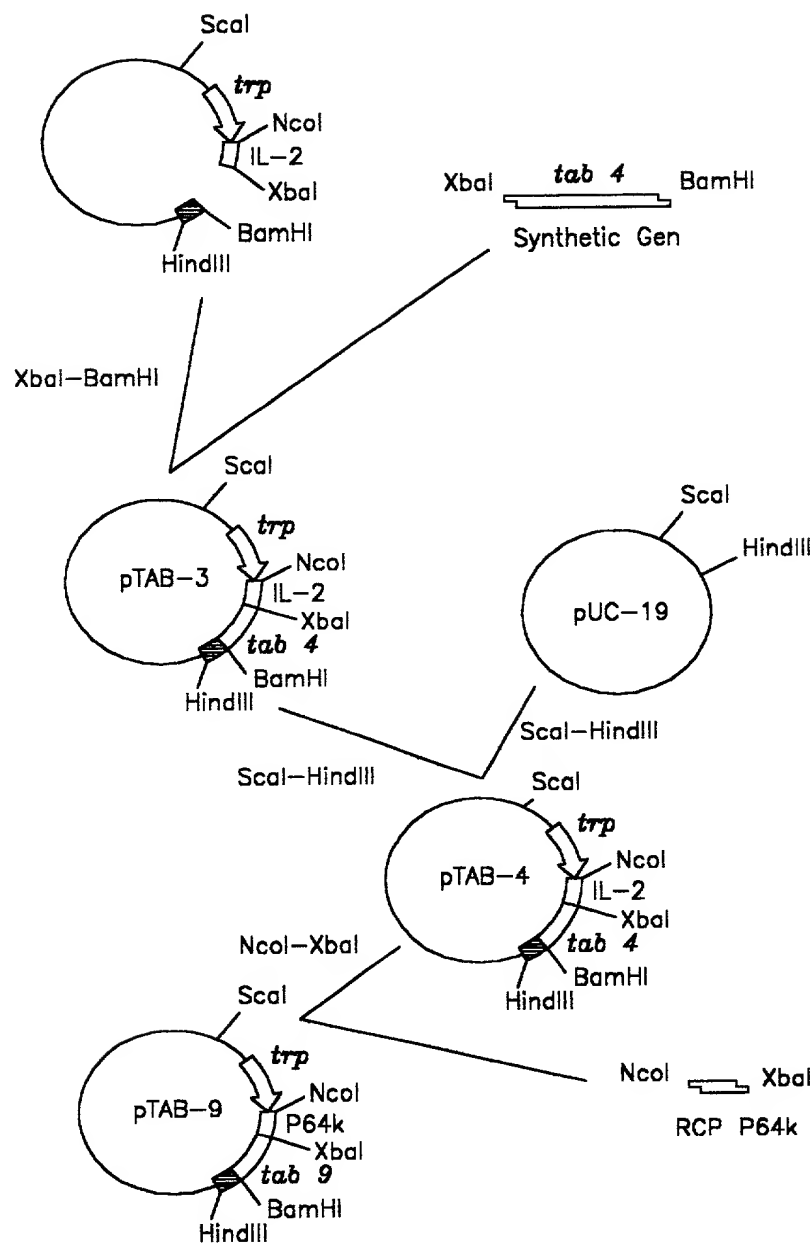


FIG. 7

FIG. 8

M V D K R M A L V E L K V P D I G G H
 ATG GTA GAT AAA AGA ATG GCT TTA GTT GAA TTG AAA GTG CCC GAC ATT GGC GGA CAC
 E N V D I I A V E V N V G D T I A V D
 AA AAT GTA GAT ATT ATC GCG GTT GAA GTA AAC GTG GGC GAC ACT ATT GCT GTG GAC
 D T L I T L D L D S R G I R I G P G R
 GAT ACC CTG ATT ACT TTG GAT CTA GAC TCG AGA GGC ATT CGT ATC GGC CCA GGT CGC
 A I L A T A G G G A R Q S T P I G L G
 GCA ATT TTA GCA ACA GCT GGC GGT GGC GCA CGT CAA TCT ACC CCT ATT GGT TTA GGT
 G A L Y T T A G G G A R K S I T K G P
 CAG GCT CTG TAT ACG ACT GCC GGC GGT GGT GCG CGC AAA AGT ATC ACC AAG GGT CCA
 G R V I Y A T A G G A R K R I H I G
 GGC CGC GTC ATT TAC GCC ACC GCG GGC GGC GGT GCC CGT AAG CGT ATC CAC ATT GGC
 P G R A F Y T T A G G G A R K R I T M
 CCA GGC CGT GCA TTC TAT ACT ACA GCA GGT GGT GGC GCA CGT AAA CGC ATC ACT ATG
 G P G R V Y Y T T A G G G A S I R I Q
 GGT CCT GGT CGC GTC TAT TAC ACG ACC GCT GGC GGC GGT GCT AGC ATT CGC ATC CAA
 R G P G R A F V T I *
 CGC GGC CCT GGT CGT GCA TTT GTG ACC ATA TGA

CGC GGC CCT GGT CGT GCA TTT GTG ACC ATA TGA

FIG. 9A

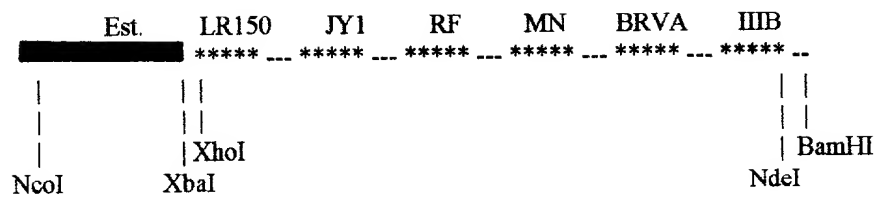


FIG. 9B

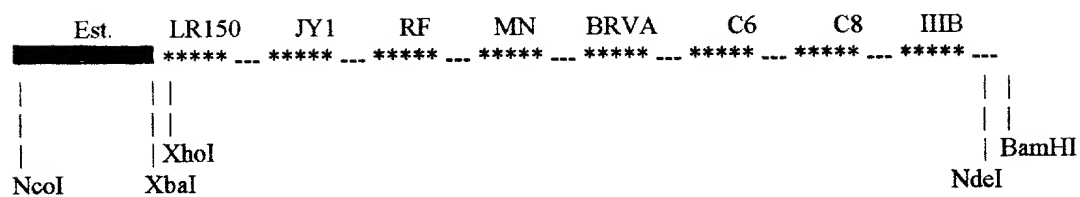


FIG. 10A

Gene	Stabilizer	Plasmid	Culture medium	% of expression
<i>porA</i>	hIL2-58	pILM-28	M9	32
	P64k-47	pM-82	M9	34
<i>opc</i>	hIL2-58	pILM-29	M9	25
	P64k-47	pM-80	M9	20
TAB	hIL2-22	pTAB4	LB	5
	P64k-47	pTAB4	LB	10

FIG. 10B

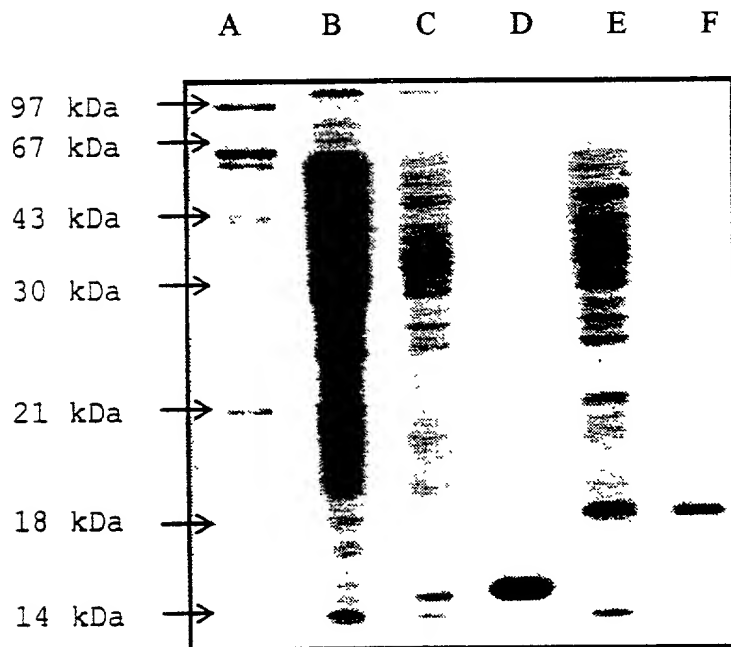


FIG. 10C

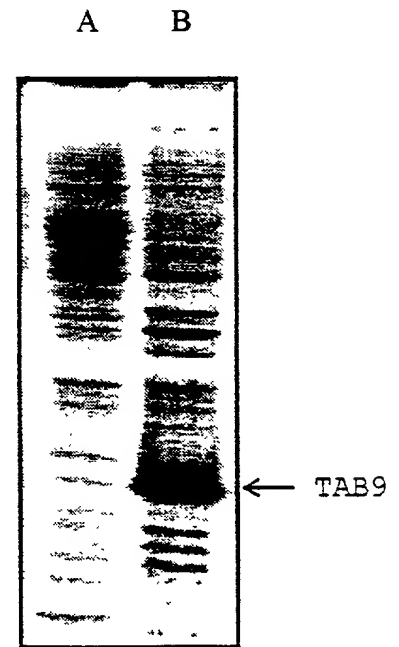


FIG. 11

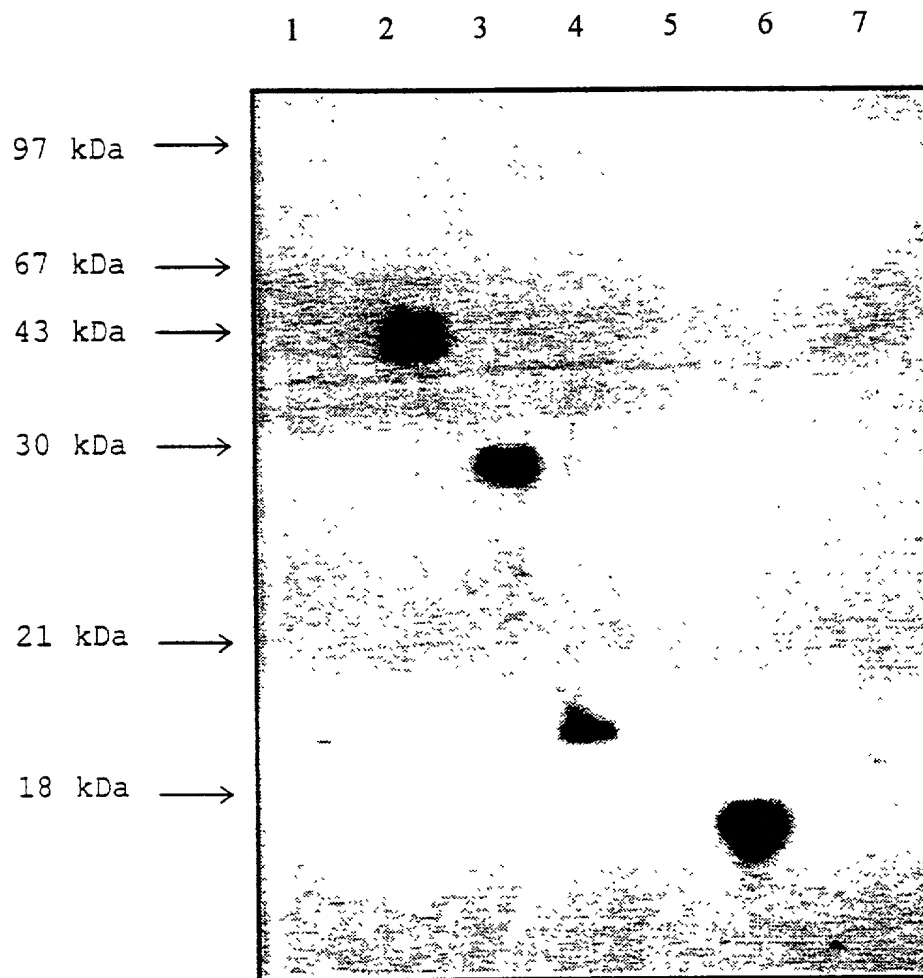


FIG. 12

	TAB 4				TAB 9			
RABBIT#	12166	5725	5340	2310	1	2	3	10
TAB	20480	10240	10240	81920	20480	20480	51200	51200
	0	0	0	0	0	0		
LR150	<100	<100	<100	6400	400	<100	800	<100
JY1	200	<100	<100	12800	1600	6400	3200	<100
RF	6400	<100	3200	800	<100	200	3200	800
MN	200	<100	<100	1600	1600	3200	6400	<100
BRVA	<100	6400	400	3200	800	400	6400	1600
IIIB	<100	<100	<100	<100	800	<100	800	<100
GM	1820				1416			
R%	45.8%				75%			

**UNITED STATES -- PATENT
DECLARATION FOR PATENT APPLICATION**

Attorney's Docket No.: P-13

As a below-named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below), or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

EXPRESSION SYSTEM OF HETEROLOGOUS ANTIGENS AS FUSION PROTEINS

the specification of which
(check one) ☒ X is attached hereto.

☐ was filed on _____ as

Application Serial No.: _____,

and was amended on _____
(if applicable)

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any Amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, §119 and/or §371, of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the Application on which priority is claimed:

Prior Foreign Application(s):

Appln. No.	Country	Date Filed	Priority Claimed
PCT/CU97/00001	PCT	1/17/97	<input checked="" type="checkbox"/> YES <input type="checkbox"/> NO
CU 10/96	Cuba	1/17/96	<input checked="" type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO

I hereby claim the benefit under Title 35, United States Code, §120 of any United States Application(s) listed below and, insofar as the subject matter of each of the claims of this Application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code §112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, §1.56(a) which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Appln. Serial No.	Filing Date	Status: Patented, Pending, Abandoned
		<input type="checkbox"/> Patented <input type="checkbox"/> Pending <input type="checkbox"/> Abandoned
		<input type="checkbox"/> Patented <input type="checkbox"/> Pending <input type="checkbox"/> Abandoned
		<input type="checkbox"/> Patented <input type="checkbox"/> Pending <input type="checkbox"/> Abandoned

POWER OF ATTORNEY

I hereby appoint the following attorney(s) and/or agent(s) to prosecute the application entitled,

EXPRESSION SYSTEM OF HETEROLOGOUS ANTIGENS AS FUSION PROTEINS

and to transact all business in the Patent and Trademark Office connected therewith:

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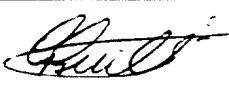
HOWARD N. ARONSON, Reg. No. 27,302; and

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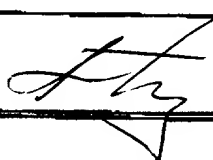
I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.


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Date 4/9/97	Signature 


X Additional inventors are being named on separately numbered sheets attached hereto.

PA2

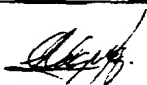
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Date 4-9-97	Signature 

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Date 4-9-97	Signature 

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Date 4-9-97	Signature 

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State or Country CUBA	State or Country CUBA
Date 4-9-97	Signature 

Full Name of First or Sole Inventor	Citizenship
RESIDENCE Address -- Street	POST OFFICE Address -- Street
City (Zip)	City (Zip)
State or Country	State or Country
Date	Signature

SEQUENCE LISTING

SEQUENCE IDENTIFICATION NO.: 1

SEQUENCE TYPE: amino acid

LENGTH: 47 amino acids

MOLECULE TYPE: protein fragment.

PROPERTIES: First 47 amino acids of the recombinant protein P64k of *N. meningitidis*.

MLDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETD

44

SEQUENCE IDENTIFICATION NO.: 2

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 5' No. 1573 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTCCATGGTAGATAAAAGAATGGCTTTAG

29

SEQUENCE IDENTIFICATION NO.: 3

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 1575 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTTCTAGATCCAAAGTAATCAGGGTATCG

29

SEQUENCE IDENTIFICATION NO.: 4

SEQUENCE TYPE: Nucleotide

LENGTH: 26 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 2192 for PCR amplification of the first 120 amino acids from the P64k antigen of *N. meningitidis*.

GGCGGTTCTGCCGATTAAGGATCCGA

26

SEQUENCE IDENTIFICATION NO.: 5

SEQUENCE TYPE: Nucleotide

LENGTH: 146 base pairs

MOLECULE TYPE: PCR amplified fragment

PROPERTIES: Derived fragment from the first 47 amino acids of the P64k antigen of *N. meningitidis*. Restriction sites NcoI (positions 3 to 8) and XbaI (positions 139 to 144) are introduced by PCR, which provoke changes in the nucleotide sequence of this fragment.

TTCCATGGTAGATAAAAAGAATGGCTTTAGTTGAATTGAAAGTGCCCGACATTGGCGGACA 60
CGAAAATGTAGATATTATCGCGGTTGAAGTAAACGTGGGCGACACTATTGCTGTGGACGA 120
TACCCTGATTACTTTGGATCTAGAAA 146

SEQUENCE IDENTIFICATION NO.: 6
SEQUENCE TYPE: amino acid
LENGTH: 47 amino acids
MOLECULE TYPE: stabiliser fragment derived from the first 47 amino acids of the P64k antigen of *N. meningitidis*.
PROPERTIES: This fragment has the following changes with respect to the P64k. L2→V2; E45→D45; T46→L46; D47→E47

MVDKRMALVELKVPDIGGHENVDIHAVEVNVGDTIAVDDTLITLDLE 47

SEQUENCE IDENTIFICATION NO.: 7
SEQUENCE TYPE: Nucleotide
LENGTH: 16 bases
MOLECULE TYPE: Synthetic oligonucleotide

CTAGATTTGATATCAG 16

SEQUENCE IDENTIFICATION NO.: 8
SEQUENCE TYPE: Nucleotide
LENGTH: 16 bases
MOLECULE TYPE: Synthetic oligonucleotide

GATCCTGATATCAAAT 16

SEQUENCE IDENTIFICATION NO.: 9
SEQUENCE TYPE: amino acid
LENGTH: 15 amino acids
MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1. LR150 isolate.

SRGIRIGPGRILAT 15

SEQUENCE IDENTIFICATION NO.: 10

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, JY1 isolate.

RQSTPIGLGQALYTT

15

SEQUENCE IDENTIFICATION NO.: 11

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, RF isolate.

RKSITKGPRVIYAT

15

SEQUENCE IDENTIFICATION NO.: 12

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, MN isolate.

RKRIHIGPGRAFYTT

15

SEQUENCE IDENTIFICATION NO.: 13

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, BRVA isolate.

RKRITMGPRVYYTT

15

SEQUENCE IDENTIFICATION NO.: 14

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, IIIB isolate.

SIRIQRGPGRAFVTI

15

SEQUENCE IDENTIFICATION NO.: 15

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: Consensus sequence of the central region of the V3 loop from the gp120 protein of different HIV-1 isolates, position 7 within the MEP TAB13.

TSITIGPGQVFYRTG

15

SEQUENCE IDENTIFICATION NO.: 16

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: Consensus sequence of the central region of the V3 loop from the gp120 protein of different HIV-1 isolates, position 8 within the MEP TAB13.

RQRTSIGQGQALYTT

15

SEQUENCE IDENTIFICATION NO.: 17

SEQUENCE TYPE: amino acid

LENGTH: 5 amino acids

MOLECULE TYPE: flexible linker that divides the V3 epitopes in the MEP TAB3, TAB4, TAB9 and TAB13.

AGGGA

5

SEQUENCE IDENTIFICATION NO.: 18

SEQUENCE TYPE: amino acid

LENGTH: 141 amino acids

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB4.

MAPTSSSTAQTQLQLEHLLLDLQIFLSRGIRIGPGRAILATAGGGARQSTPIGLGGALYT 60

TAGGGARKSITKGPRVIYATAGGGARKRIHIGPGRAFYT TAGGGARKRITMGPRVYYT 120

TAGGGASIRIQRGPGRAFVTI 141

SEQUENCE IDENTIFICATION NO.: 19

SEQUENCE TYPE: amino acid

LENGTH: 162 amino acids

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB9.

MVDKRMALVELKVPDIGGHENVDIHAVEVNVGDTIAVDDTLITLDLDSRGIRIGPGRAIL 60
ATAGGGARQSTPIGLGGALYTTAGGGARKSITKGPGRVIYATAGGGARKRIHIGPGRAFY 120
TTAGGGARKRITMGPRVYYTTAGGGASIRIQRGPGRAFTI 162

SEQUENCE IDENTIFICATION NO.: 20
SEQUENCE TYPE: amino acid
LENGTH: 202 amino acids
MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB13.

MVDKRMALVELKVPDIGGHENVDIHAVEVNVGDTIAVDDTLITLDLDSRGIRIGPGRAIL 60
ATAGGGAROSTPIGLGOALYTTAGGGARKSITKGPGRVIYATAGGGARKRIHIGPGRAFY 120
TTAGGGARKRITMGPRVYYTTAGGGARORTSIGOGOALYTTAGGGATSITIGPGOVFYR 180
TGAGGGASIRIQRGPGRAFTI 202

SEQUENCE IDENTIFICATION NO.: 21
SEQUENCE TYPE: Nucleotide
LENGTH: 368 base pairs
MOLECULE TYPE: Synthetic oligonucleotide
PROPERTIES: Nucleotide fragment that codifies for the V3 epitopes bound by a AGGGA spacer in the MEP TAB9. Restriction sites XbaI (positions 1 to 6) and BamHI (positions 363 to 368) are introduced.

TCTAGACTCGAGAGGCATTTCGTATCGGCCAGGTCGCGCAATTTAGCAACAGCTGGCGG 60
TGGCGCACGTCAATCTACCCCTATTGGTTTAGGTCAGGCTCTGTATACGACTGCCGGCGG 120
TGGTGC GCGCAAAAGTATCACCAAGGGTCCAGGCCGCGTCATTTACGCCACCGCGGGCGG 180
CGGTGCCCCGTAAGCGTATCCACATTGGCCCAGGCCGTGCATTCTATACTACAGCAGGTGG 240
TGGCGCACGTAAACGCATCACTATGGGTCCTGGTCGCGTCTATTACACGACCGCTGGCGG 300
CGGTGCTAGCATTGCGATCCAACGCGGCCCTGGTCGTGCATTTGTGACCATATGATAACG 360
CGGGATCC 368

[illegible]

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(C) OPERATING SYSTEM: Windows 95.
(D) SOFTWARE: Word Perfect 5.0 for Windows 95.

(A) APPLICATION NUMBER: 08/930,917
(B) FILING DATE: 16-Sep-1997
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: PCT/CU97/00001
(B) FILING DATE: 17-Jan-1997

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(2) INFORMATION FOR SEQ. ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: First 47 amino acids of the recombinant protein of Neisseria

meningitidis P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp

35 40 45

(2) INFORMATION FOR SEQ. ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1573

(D) OTHER INFORMATION: Primer 5' for PCR amplification of the first 44 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
TTCCATGGTA GATAAAAGAA TGGCTTTAG

29

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1575

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTCTAGATC CAAAGTAATC AGGGTATCG

29

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: Primer 2192

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 120 amino acids of the

recombinant protein of Neisseria meningitidis P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
GGCGGTTCTG CCGATTAAGG ATCCGA

26

CGCGGTTCTG CCGATTAAGG ATCCGA

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Fragment amplified by PCR

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Fragment derived from the first 47 amino acids of the recombinant protein of Neisseria meningitidis P64K, containing a NcoI site at the position 3 to 8 and a XbaI site at the position 139 to 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCCATGGTA GATAAAAGAA TGGCTTTAGT TGAATTGAAA GTGCCCGACA
TTGGCGGACA 60

CGAAAATGTA GATATTATCG CGGTTGAAGT AACGTGGGC GACACTATTG
CTGTGGACGA 120

TACCCTGATT ACTTTGGATC TAGAAA
146

(2) INFORMATION FOR SEQ. ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues
(B) TYPE: Amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Stabilizer derived from the first 47 amino acids of the recombinant

protein of *Neisseria meningitidis* P64K, containing the following changes: L2 V2; E45 D45;

T46 L46; D47 E47.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu

35 40 45

(2) INFORMATION FOR SEQ. ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

[illegible]

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(B) STRAIN: B:4:P1.15

(B) CLONE: P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :
CTAGATTGTA TATCAG

16

(D) TOPOLOGY: Unknown

(A)DESCRIPTION: Synthetic oligonucleotide

(iv) ANTI-SENSE: No

(B) STRAIN: B:4:P1.15.

(B) CLONE: P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

[illegible]

(2) INFORMATION FOR SEQ. ID NO: 9:

(A) LENGTH: 15 Amino acid residues

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: LR150

(ix) **FEATURE:**

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the

VIH-1, isolation LR150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ser Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr

1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 10:

(A) SEQUENCE CHARACTERISTICS:

(B) LENGTH: 15 Amino acid residues

(C) TYPE: Amino acid

(D) STRANDEDNESS: Unknown

(E) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: JY1

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation JY1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: RF

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

VIH-1, isolation BRVA.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Arg Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: IIIB

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation IIIB.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

(C) STRANDEDNESS: Unknown.

(D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging

to the protein gp120 obtained from different isolations of the VIH-1, position 7 within the

multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

[illegible]

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Arg Leu Tyr Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Flexible spacer separating epitopes V3 in the MEP
TAB3, TAB4,
TAB9 and TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala Gly Gly Gly Ala
1 5

(2) INFORMATION FOR SEQ. ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB4.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ala Pro Thr Ser Ser Ser Thr Ala Gln Thr Gln Leu Gln Leu Glu
1 5 10 15
His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile
20 25 30
Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Gly Ala Arg Gln
35 40 45
Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr Thr Thr Ala Gly Gly
50 55 60
Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala
65 70 75 80
Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg
85 90 95
Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile Thr Met
100 105 110
Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Gly Ala Ser Ile
115 120 125
Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
130 135 140

(2) INFORMATION FOR SEQ. ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB9.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile
1 5 10 15

[illegible]

(2) INFORMATION FOR SEQ. ID NO: 20:

(A) LENGTH: 202 Amino acid residues

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment.

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) **FEATURE:**

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15
 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
 20 25 30
 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser
 35 40 45
 Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly
 50 55 60

Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr
 65 70 75 80
 Thr Thr Ala Gly Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly
 85 90 95
 Arg Val Ile Tyr Ala Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His
 100 105 110
 Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg
 115 120 125
 Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly
 130 135 140
 Gly Gly Ala Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Ala Leu Tyr
 145 150 155 160
 Thr Thr Ala Gly Gly Gly Ala Thr Ser Ile Thr Ile Gly Pro Gly Gln
 165 170 175
 Val Phe Tyr Arg Thr Gly Ala Gly Gly Gly Ala Ser Ile Arg Ile Gln
 180 185 190
 Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
 195 200

(2) INFORMATION FOR SEQ. ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

OTHER INFORMATION: Codifies for epitopes V3 linked by the spacer of SEQ ID
NO: 17: in the
MEP TAB 19.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTAGACTCG AGAGGCATTC GTATCGGCCC AGGTCGCGCA
ATTTTAGCAA CAGCTGGCGG 60

TGGCGCACGT CAATCTACCC CTATTGGTTT AGGTCAGGCT
CTGTATACGA CTGCCGGCGG 120

TGGTGCGCGC AAAAGTATCA CCAAGGGTCC AGGCCGCGTC
ATTTACGCCA CCGCGGGCGG 180

CGGTGCCCCG AAGCGTATCC ACATTGGCCC AGGCCGTGCA
TTCTATACTA CAGCAGGTGG 240

TGGCGCACGT AAACGCATCA CTATGGGTCC TGGTCGCGTC
TATTACACGA CCGCTGGCGG 300

CGGTGCTAGC ATTCGCATCC AACGCGGCCC TGGTCGTGCA
TTTGTGACCA TATGATAACG 360

CGGGATCC

368